



SEQUENCE LISTING

<110> Zastawny, Roman

<120> G PROTEIN COUPLED RECEPTOR A4

<130> 2931-104

<140> US 10/060369

<141> 2002-02-01

<150> US 09/173565

<151> 1998-08-16

<160> 12

<170> PatentIn version 3.2

<210> 1

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> PCR primer

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gagacataat ggtgatggct aggaccca

28

<210> 2

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<213> Artificial Sequence

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<223> PCR primer

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ctgcgacaga tattccctgg accaatcc

28

<210> 3

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> PCR primer

<400> 3

ccatcctaatac acgactcact ataggc

26

<210> 4

<211> 23
<212> DNA
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actcactata gggctcgagc ggc

23

<210> 5
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ggcattcgaa ttcgcccggcca ccatgaatga gaaatgggac acaaactctt

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<210> 6
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<213> Artificial Sequence

<220>
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<400> 6
aggattatca ctcttagatct ttttaaatct cactgctgtt agtagttct

50

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<400> 7
tggcacgtgg tgtccaggaa gaagcag

27

<210> 8
<211> 1440
<212> DNA
<213> Human

<400> 8
ttgagccggc agactgcgaa aagttagctgg agccggagca gggacagaac ctgttgctgc

60

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| agacgggctt | ggtggattct | ggtcctgcc | gccgacaggg | ctcgccggga | gaggttcatc | 120 |
| atgaatgaga | aatgggacac | aaactcttca | gaaaactggc | atcccatctg | aatgtcaat | 180 |
| gacacaaagc | atcatctgta | ctcagatatt | aatattacct | atgtgaacta | ctatctcac | 240 |
| cagcctcaag | tggcagcaat | cttcatttatt | tcctactttc | tgatcttctt | tttgtgcatt | 300 |
| atggaaata | ctgtggtttg | ctttatttta | atgaggaaca | aacatatgca | cacagtca | 360 |
| aatctttca | tcttaaacct | ggccataagt | gatttactag | ttggcatatt | ctgcattgcct | 420 |
| ataacactgc | tggacaatat | tatagcagga | tggccatttg | gaaacacgat | gtgcaagatc | 480 |
| agtggattgg | tccagggaat | atctgtcgca | gcttcagtct | ttacgttagt | tgcaattgct | 540 |
| gtagataggt | tccagtgtgt | ggtctaccct | tttaaacc | agctcactat | caagacagcg | 600 |
| tttgtcatta | ttatgatcat | ctgggtccta | gccatcacca | ttatgtctcc | atctgcagta | 660 |
| atgttacatg | tgcaagaaga | aaaatattac | cgagtgagac | tcaactccc | gaataaaaacc | 720 |
| agtccagct | actggtgccg | ggaagactgg | ccaaatcagg | aaatgaggaa | gatctacacc | 780 |
| actgtgctgt | ttgccaacat | ctacctggct | cccctctccc | tcattgtcat | catgtatgga | 840 |
| aggattggaa | tttcaacttt | cagggctgca | gttcctcaca | caggcaggaa | gaaccaggag | 900 |
| cagtggcacg | tggtgtccag | gaagaagcag | aagatcatta | agatgctcct | gattgtggcc | 960 |
| ctgctttta | ttctctcatg | gctccccctg | tggactctaa | tgatgctctc | agactacgct | 1020 |
| gacctttctc | caaataact | gcagatcatc | aacatctaca | tctacccttt | tgcacactgg | 1080 |
| ctggcattcg | gcaacagcag | tgtcaatccc | atcatttatg | gtttttcaa | cgagaatttc | 1140 |
| cggcgtggtt | tccaagaagc | tttccagctc | cagctctgcc | aaaaaagagc | aaagcctatg | 1200 |
| gaagcttata | ccctaaaagc | taaaagccat | gtgctcataa | acacatctaa | ttagcttgc | 1260 |
| caggaatcta | catttcaaaa | ccctcatggg | gaaaccttgc | tttataggaa | aagtgctgaa | 1320 |
| aaaccccaac | aggaatttagt | gatggaagaa | ttaaaagaaa | ctactaacag | cagtgagatt | 1380 |
| taaaaagagc | tagtgtgata | atcctaactc | tactacgcat | tatatattta | aatccattgc | 1440 |

<210> 9
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<213> Human

<400> 9

Met Asn Glu Lys Trp Asp Thr Asn Ser Ser Glu Asn Trp His Pro Ile

1

5

10

15

Trp Asn Val Asn Asp Thr Lys His His Leu Tyr Ser Asp Ile Asn Ile
 20 25 30

Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala Ala Ile Phe
 35 40 45

Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys Met Met Gly Asn Thr
 50 55 60

Val Val Cys Phe Ile Val Met Arg Asn Lys His Met His Thr Val Thr
 65 70 75 80

Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu Val Gly Ile
 85 90 95

Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala Gly Trp Pro
 100 105 110

Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu Val Gln Gly Ile Ser
 115 120 125

Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Asp Arg Phe
 130 135 140

Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Ile Lys Thr Ala
 145 150 155 160

Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala Ile Thr Ile Met Ser
 165 170 175

Pro Ser Ala Val Met Leu His Val Gln Glu Glu Lys Tyr Tyr Arg Val
 180 185 190

Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val Tyr Trp Cys Arg Glu
 195 200 205

Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr Thr Thr Val Leu Phe
 210 215 220

Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile Met Tyr Gly
 225 230 235 240

Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val Pro His Thr Gly Arg
 245 250 255

Lys Asn Gln Glu Gln Trp His Val Val Ser Arg Lys Lys Gln Lys Ile
 260 265 270

Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe Ile Leu Ser Trp Leu
 275 280 285

Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Ala Asp Leu Ser Pro
 290 295 300

Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr Pro Phe Ala His Trp
 305 310 315 320

Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile Ile Tyr Gly Phe Phe
 325 330 335

Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala Phe Gln Leu Gln Leu
 340 345 350

Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr Thr Leu Lys Ala Lys
 355 360 365

Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln Glu Ser Thr
 370 375 380

Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr Arg Lys Ser Ala Glu
 385 390 395 400

Lys Pro Gln Gln Glu Leu Val Met Glu Glu Leu Lys Glu Thr Thr Asn
 405 410 415

Ser Ser Glu Ile
 420

<210> 10
 <211> 384
 <212> PRT

<213> Human

<400> 10

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Ser | Thr | Leu | Phe | Ser | Gln | Val | Glu | Asn | His | Ser | Val | His | Ser |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Phe | Ser | Glu | Lys | Asn | Ala | Gln | Leu | Leu | Ala | Phe | Glu | Asn | Asp | Asp |
| | | | | 20 | | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | His | Leu | Pro | Leu | Ala | Met | Ile | Phe | Thr | Leu | Ala | Leu | Ala | Tyr | Gly |
| | | | | | | 35 | | 40 | | | | | 45 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Val | Ile | Ile | Leu | Gly | Val | Ser | Gly | Asn | Leu | Ala | Leu | Ile | Ile | Ile |
| | | | | | | 50 | | | | 55 | | | 60 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Leu | Lys | Gln | Lys | Glu | Met | Arg | Asn | Val | Thr | Asn | Ile | Leu | Ile | Val |
| | | | | | | 65 | | 70 | | 75 | | | 80 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Ser | Phe | Ser | Asp | Leu | Leu | Val | Ala | Ile | Met | Cys | Leu | Pro | Phe |
| | | | | | | 85 | | | 90 | | | | 95 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Val | Tyr | Thr | Leu | Met | Asp | His | Trp | Val | Phe | Gly | Glu | Ala | Met |
| | | | | | | 100 | | | 105 | | | | 110 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Lys | Leu | Asn | Pro | Phe | Val | Gln | Cys | Val | Ser | Ile | Thr | Val | Ser | Ile |
| | | | | | | | | 115 | | 120 | | | 125 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ser | Leu | Val | Leu | Ile | Ala | Val | Glu | Arg | His | Gln | Leu | Ile | Ile | Asn |
| | | | | | | | | 130 | | 135 | | | 140 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Arg | Gly | Trp | Arg | Pro | Asn | Asn | Arg | His | Ala | Tyr | Val | Gly | Ile | Ala |
| | | | | | | 145 | | | 150 | | | 155 | | | 160 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Trp | Val | Leu | Ala | Val | Ala | Ser | Ser | Leu | Pro | Phe | Leu | Ile | Tyr |
| | | | | | | | | 165 | | 170 | | | 175 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Met | Thr | Asp | Glu | Pro | Phe | Gln | Asn | Val | Thr | Leu | Asp | Ala | Tyr |
| | | | | | | | | 180 | | 185 | | | 190 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asp | Lys | Tyr | Val | Cys | Phe | Asp | Gln | Phe | Pro | Ser | Asp | Ser | His | Arg |
| | | | | | | | | 195 | | 200 | | | 205 | | |

Leu Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu
 210 215 220

Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg
 225 230 235 240

Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser
 245 250 255

Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe
 260 265 270

Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp
 275 280 285

Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu
 290 295 300

Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr
 305 310 315 320

Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn
 325 330 335

Phe Cys Asp Phe Arg Ser Arg Asp Asp Tyr Glu Thr Ile Ala Met
 340 345 350

Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser
 355 360 365

Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn Glu Lys Ile
 370 375 380

<210> 11
 <211> 444
 <212> PRT
 <213> Human

<400> 11

Met Ser Gly Thr Lys Leu Glu Asp Ser Pro Pro Cys Arg Asn Trp Ser
 1 5 10 15

Ser Ala Ser Glu Leu Asn Glu Thr Gln Glu Pro Phe Leu Asn Pro Thr
 20 25 30

Asp Tyr Asp Asp Glu Glu Phe Leu Arg Tyr Leu Trp Arg Glu Tyr Leu
 35 40 45

His Pro Lys Glu Tyr Glu Trp Val Leu Ile Ala Gly Tyr Ile Ile Val
 50 55 60

Phe Val Val Ala Leu Ile Gly Asn Val Leu Val Cys Val Ala Val Trp
 65 70 75 80

Lys Asn His His Met Arg Thr Val Thr Asn Tyr Phe Ile Val Asn Leu
 85 90 95

Ser Leu Ala Asp Val Leu Val Thr Ile Thr Cys Leu Pro Ala Thr Leu
 100 105 110

Val Val Asp Ile Thr Glu Thr Trp Phe Phe Gly Gln Ser Leu Cys Lys
 115 120 125

Val Ile Pro Tyr Leu Gln Thr Val Ser Val Ser Val Val Leu Thr
 130 135 140

Leu Ser Cys Ile Ala Leu Asp Arg Trp Tyr Ala Ile Cys His Pro Leu
 145 150 155 160

Met Phe Lys Ser Thr Ala Lys Arg Ala Arg Asn Ser Ile Val Ile Ile
 165 170 175

Trp Ile Val Ser Cys Ile Ile Met Ile Pro Gln Ala Ile Val Met Glu
 180 185 190

Cys Ser Thr Val Phe Pro Gly Leu Ala Asn Lys Thr Thr Leu Phe Thr
 195 200 205

Val Cys Asp Glu Arg Trp Gly Gly Glu Ile Tyr Pro Lys Met Tyr His
 210 215 220

Ile Cys Phe Phe Leu Val Thr Tyr Met Ala Pro Leu Cys Leu Met Val
 225 230 235 240

Leu Ala Tyr Leu Gln Ile Phe Arg Lys Leu Trp Cys Arg Gln Ile Pro
 245 250 255

Gly Thr Ser Ser Val Val Gln Arg Lys Trp Lys Pro Leu Gln Pro Val
 260 265 270

Ser Gln Pro Arg Gly Pro Gly Gln Pro Thr Lys Ser Arg Met Ser Ala
 275 280 285

Val Ala Ala Glu Ile Lys Gln Ile Arg Ala Arg Arg Lys Thr Ala Arg
 290 295 300

Met Leu Met Val Val Leu Leu Val Phe Ala Ile Cys Tyr Leu Pro Ile
 305 310 315 320

Ser Ile Leu Asn Val Leu Lys Arg Val Phe Gly Met Phe Ala His Thr
 325 330 335

Glu Asp Arg Glu Thr Val Tyr Ala Trp Phe Thr Phe Ser His Trp Leu
 340 345 350

Val Tyr Ala Asn Ser Ala Ala Asn Pro Ile Ile Tyr Asn Phe Leu Ser
 355 360 365

Gly Lys Phe Arg Glu Glu Phe Lys Ala Ala Phe Ser Cys Cys Cys Leu
 370 375 380

Gly Val His His Arg Gln Glu Asp Arg Leu Thr Arg Gly Arg Thr Ser
 385 390 395 400

Thr Glu Ser Arg Lys Ser Leu Thr Thr Gln Ile Ser Asn Phe Asp Asn
 405 410 415

Ile Ser Lys Leu Ser Glu Gln Val Val Leu Thr Ser Ile Ser Thr Leu
 420 425 430

Pro Ala Ala Asn Gly Ala Gly Pro Leu Gln Asn Trp
 435 440

<211> 428
<212> PRT
<213> Human
<400> 12

Met Asp Val Val Asp Ser Leu Leu Val Asn Gly Ser Asn Ile Thr Pro
1 5 10 15

Pro Cys Glu Leu Gly Leu Glu Asn Glu Thr Leu Phe Cys Leu Asp Gln
20 25 30

Pro Arg Pro Ser Lys Glu Trp Gln Pro Ala Val Gln Ile Leu Leu Tyr
35 40 45

Ser Leu Ile Phe Leu Leu Ser Val Leu Gly Asn Thr Leu Val Ile Thr
50 55 60

Val Leu Ile Arg Asn Lys Arg Met Arg Thr Val Thr Asn Ile Phe Leu
65 70 75 80

Leu Ser Leu Ala Val Ser Asp Leu Met Leu Cys Leu Phe Cys Met Pro
85 90 95

Phe Asn Leu Ile Pro Asn Leu Leu Lys Asp Phe Ile Phe Gly Ser Ala
100 105 110

Val Cys Lys Thr Thr Tyr Phe Met Gly Thr Ser Val Ser Val Ser
115 120 125

Thr Phe Asn Leu Val Ala Ile Ser Leu Phe Arg Tyr Gly Ala Ile Cys
130 135 140

Lys Pro Leu Gln Ser Arg Val Trp Gln Thr Lys Ser His Ala Leu Lys
145 150 155 160

Val Ile Ala Ala Thr Trp Cys Leu Ser Phe Thr Ile Met Thr Pro Tyr
165 170 175

Pro Ile Tyr Ser Asn Leu Val Pro Phe Thr Lys Asn Asn Asn Gln Thr
180 185 190

Ala Asn Met Cys Arg Phe Leu Leu Pro Asn Asp Val Met Gln Gln Ser

195

200

205

Trp His Thr Phe Leu Leu Leu Ile Leu Phe Leu Ile Pro Gly Ile Val
 210 215 220

Met Met Val Ala Tyr Gly Leu Ile Ser Leu Glu Leu Tyr Gln Gly Ile
 225 230 235 240

Lys Phe Glu Ala Ser Gln Lys Lys Ser Ala Lys Glu Arg Lys Pro Ser
 245 250 255

Thr Thr Ser Ser Gly Lys Tyr Glu Asp Ser Asp Gly Cys Tyr Leu Gln
 260 265 270

Lys Thr Arg Pro Pro Arg Lys Leu Glu Leu Arg Gln Leu Ser Thr Gly
 275 280 285

Ser Ser Ser Arg Ala Asn Arg Ile Arg Ser Asn Ser Ser Ala Ala Asn
 290 295 300

Leu Met Ala Lys Lys Arg Val Ile Arg Met Leu Ile Val Ile Val Val
 305 310 315 320

Leu Phe Phe Leu Cys Trp Met Pro Ile Phe Ser Ala Asn Ala Trp Arg
 325 330 335

Ala Tyr Asp Thr Ala Ser Ala Glu Arg Arg Leu Ser Gly Thr Pro Ile
 340 345 350

Ser Phe Ile Leu Leu Leu Ser Tyr Thr Ser Ser Cys Val Asn Pro Ile
 355 360 365

Ile Tyr Cys Phe Met Asn Lys Arg Phe Arg Leu Gly Phe Met Ala Thr
 370 375 380

Phe Pro Cys Cys Pro Asn Pro Gly Pro Pro Gly Ala Arg Gly Glu Val
 385 390 395 400

Gly Glu Glu Glu Glu Gly Gly Thr Thr Gly Ala Ser Leu Ser Arg Phe
 405 410 415

A C O S E Q E S S - Q E E K I O E

Ser Tyr Ser His Met Ser Ala Ser Val Pro Pro Gln
420 425